

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,758

DATE: 09/27/2001

TIME: 11:58:46

Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

2 <110> APPLICANT: Takeda Chemical Industries, Ltd.  
W--> 3 <120> TITLE OF INVENTION: Novel Protein and its DNA  
W--> 4 <130> FILE REFERENCE: 2568WOOP  
C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/831,758  
C--> 5 <141> CURRENT FILING DATE: 2001-08-17  
5 <150> PRIOR APPLICATION NUMBER: JP 10-323759  
6 <151> PRIOR FILING DATE: 1998-11-13  
7 <150> PRIOR APPLICATION NUMBER: JP 11-060030  
8 <151> PRIOR FILING DATE: 1999-03-08  
9 <150> PRIOR APPLICATION NUMBER: JP 11-106812  
10 <151> PRIOR FILING DATE: 1999-04-14  
11 <150> PRIOR APPLICATION NUMBER: JP 11-166672  
12 <151> PRIOR FILING DATE: 1999-06-14  
13 <150> PRIOR APPLICATION NUMBER: JP 11-221640  
14 <151> PRIOR FILING DATE: 1999-08-04  
15 <150> PRIOR APPLICATION NUMBER: JP 11-259818  
16 <151> PRIOR FILING DATE: 1999-09-14  
E--> 17 <160> NUMBER OF SEQ ID: 58

## ERRORED SEQUENCES

210 <210> SEQ ID NO: 15  
211 <211> LENGTH: 588  
212 <212> TYPE: DNA  
213 <213> ORGANISM: Bovine  
W--> 214 <400> SEQUENCE: 15  
E--> 214 15  
E--> 215 <210> SEQ ID NO: 15

*check sequence 15 for actual sequence listing*

## VERIFICATION SUMMARY

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L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:270 C: Current Application Number differs, Replaced Current Application No  
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:17 M:283 W: Missing Blank Line separator, <160> field identifier  
L:18 M:283 W: Missing Blank Line separator, <210> field identifier  
L:22 M:283 W: Missing Blank Line separator, <400> field identifier  
L:51 M:283 W: Missing Blank Line separator, <400> field identifier  
L:52 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=2  
L:65 M:283 W: Missing Blank Line separator, <220> field identifier  
L:67 M:283 W: Missing Blank Line separator, <400> field identifier  
L:68 M:112 C: (48) String data converted to lower case,  
L:73 M:283 W: Missing Blank Line separator, <220> field identifier  
L:75 M:283 W: Missing Blank Line separator, <400> field identifier  
L:76 M:112 C: (48) String data converted to lower case,  
L:81 M:283 W: Missing Blank Line separator, <220> field identifier  
L:83 M:283 W: Missing Blank Line separator, <400> field identifier  
L:84 M:112 C: (48) String data converted to lower case,  
L:89 M:283 W: Missing Blank Line separator, <220> field identifier  
L:91 M:283 W: Missing Blank Line separator, <400> field identifier  
L:92 M:112 C: (48) String data converted to lower case,  
L:97 M:283 W: Missing Blank Line separator, <220> field identifier  
L:99 M:283 W: Missing Blank Line separator, <400> field identifier  
L:100 M:112 C: (48) String data converted to lower case,  
L:105 M:283 W: Missing Blank Line separator, <400> field identifier  
L:136 M:283 W: Missing Blank Line separator, <400> field identifier  
L:137 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=9  
L:151 M:283 W: Missing Blank Line separator, <220> field identifier  
L:153 M:283 W: Missing Blank Line separator, <400> field identifier  
L:154 M:112 C: (48) String data converted to lower case,  
L:159 M:283 W: Missing Blank Line separator, <220> field identifier  
L:161 M:283 W: Missing Blank Line separator, <400> field identifier  
L:162 M:112 C: (48) String data converted to lower case,  
L:167 M:283 W: Missing Blank Line separator, <220> field identifier  
L:169 M:283 W: Missing Blank Line separator, <400> field identifier  
L:170 M:112 C: (48) String data converted to lower case,  
L:175 M:283 W: Missing Blank Line separator, <220> field identifier  
L:177 M:283 W: Missing Blank Line separator, <400> field identifier  
L:178 M:112 C: (48) String data converted to lower case,  
L:183 M:283 W: Missing Blank Line separator, <400> field identifier  
L:214 M:283 W: Missing Blank Line separator, <400> field identifier  
L:214 M:252 E: No. of Seq. differs, <211>LENGTH:Input:588 Found:0 SEQ:15  
L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:15  
L:219 M:283 W: Missing Blank Line separator, <400> field identifier  
L:220 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=15

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L:234 M:283 W: Missing Blank Line separator, <220> field identifier  
L:236 M:283 W: Missing Blank Line separator, <400> field identifier  
L:237 M:112 C: (48) String data converted to lower case,  
L:242 M:283 W: Missing Blank Line separator, <220> field identifier  
L:244 M:283 W: Missing Blank Line separator, <400> field identifier  
L:245 M:112 C: (48) String data converted to lower case,  
L:250 M:283 W: Missing Blank Line separator, <400> field identifier  
L:281 M:283 W: Missing Blank Line separator, <400> field identifier  
L:282 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=19  
L:297 M:283 W: Missing Blank Line separator, <220> field identifier  
L:299 M:283 W: Missing Blank Line separator, <400> field identifier  
L:300 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20  
L:300 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:300 M:112 C: (48) String data converted to lower case,  
L:305 M:283 W: Missing Blank Line separator, <220> field identifier  
L:307 M:283 W: Missing Blank Line separator, <400> field identifier  
L:308 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21  
L:308 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:308 M:112 C: (48) String data converted to lower case,  
L:313 M:283 W: Missing Blank Line separator, <220> field identifier  
L:315 M:283 W: Missing Blank Line separator, <400> field identifier  
L:316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22  
L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:316 M:112 C: (48) String data converted to lower case,  
L:321 M:283 W: Missing Blank Line separator, <220> field identifier  
L:323 M:283 W: Missing Blank Line separator, <400> field identifier  
L:324 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23  
L:324 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:324 M:112 C: (48) String data converted to lower case,  
L:329 M:283 W: Missing Blank Line separator, <220> field identifier  
L:331 M:283 W: Missing Blank Line separator, <400> field identifier  
L:332 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24  
L:332 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:332 M:112 C: (48) String data converted to lower case,  
L:337 M:283 W: Missing Blank Line separator, <220> field identifier  
L:339 M:283 W: Missing Blank Line separator, <400> field identifier  
L:340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25  
L:340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25  
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:340 M:112 C: (48) String data converted to lower case,  
L:345 M:283 W: Missing Blank Line separator, <220> field identifier  
L:347 M:283 W: Missing Blank Line separator, <400> field identifier  
L:348 M:112 C: (48) String data converted to lower case,

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Input Set : A:\Sequence Listing .txt

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L:353 M:283 W: Missing Blank Line separator, <220> field identifier  
L:356 M:112 C: (48) String data converted to lower case,  
L:364 M:112 C: (48) String data converted to lower case,  
L:372 M:112 C: (48) String data converted to lower case,  
L:380 M:112 C: (48) String data converted to lower case,  
L:388 M:112 C: (48) String data converted to lower case,  
L:396 M:112 C: (48) String data converted to lower case,  
L:431 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=34  
L:448 M:112 C: (48) String data converted to lower case,  
L:456 M:112 C: (48) String data converted to lower case,  
L:521 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=38  
L:575 M:112 C: (48) String data converted to lower case,  
L:581 M:112 C: (48) String data converted to lower case,  
L:587 M:112 C: (48) String data converted to lower case,  
L:593 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=45  
L:603 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=46  
L:614 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=47  
L:628 M:112 C: (48) String data converted to lower case,  
L:636 M:112 C: (48) String data converted to lower case,  
L:673 M:112 C: (48) String data converted to lower case,  
L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (58) Counted (59)

STATISTICS SUMMARY

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Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

Application Serial Number: US/09/831,758

Alpha or Numeric: Numeric

Application Class:

Application File Date: 08-17-2001

Art Unit: PCT09

Software Application:

Total Number of Sequences: 59

Total Nucleotides: 9253

Total Amino Acids: 2059

Number of Errors: 3

Number of Warnings: 116

Number of Corrections: 362

MESSAGE SUMMARY

112 C: 180 ((48) String data converted to lower case)  
203 E: 1 (No. of Seq. differs)  
212 E: 1 ((34) Invalid or duplicate Sequence ID Number)  
252 E: 1 (No. of Seq. differs)  
258 W: 12 (Mandatory Feature missing)  
270 C: 1 (Current Application Number differs)  
271 C: 1 (Current Filing Date differs)  
283 W: 98 (Missing Blank Line separator)  
341 W: 6 ((46) "n" or "Xaa" used)